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09/28/01

OIPE

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/09/724,126A**

DATE: 07/16/2001  
TIME: 14:15:51

Input Set : A:\35966Aseq.txt  
Output Set: N:\CRF3\07162001\I724126A.raw

P. 5

5 <110> APPLICANT: Han, Hui-Quan  
6 Kwak, Keith  
9 <120> TITLE OF INVENTION: Human E3 Alpha Ubiquitin Ligase Family  
11 <130> FILE REFERENCE: 01017/35966A  
13 <140> CURRENT APPLICATION NUMBER: US 09/724,126A  
14 <141> CURRENT FILING DATE: 2000-11-28  
16 <150> PRIOR APPLICATION NUMBER: US 60/187,211  
17 <151> PRIOR FILING DATE: 1999-03-01  
19 <160> NUMBER OF SEQ ID NOS: 29  
21 <170> SOFTWARE: PatentIn version 3.0  
23 <210> SEQ ID NO: 1  
24 <211> LENGTH: 6308  
25 <212> TYPE: DNA  
26 <213> ORGANISM: Homo sapiens  
28 <220> FEATURE:  
29 <221> NAME/KEY: CDS  
30 <222> LOCATION: (696)..(5942)  
32 <400> SEQUENCE: 1  
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37 ccaaaggctt atcatctgtc ttccacttat ccaacaagct gctatggcca ctgcctgtg  
39 cgcacctgga accaccgcca gccccactac tgcctccact accactgggtt ctcccaccc  
41 gatcagctgc ttgctgctgc catcttatacc gtttctgcct gttctgagta aatgtatacc  
43 caccctggaa accaccattc tactttctgt gtctatgaat ttgactactc tagctggat  
45 ccgagctttt ttgtacacat gtgcaagtgc ccacgggta gaatcctaaa aatagaaga  
47 gtatgcaaca gttcccagca ccaaaccacca atatacaacc attcagctac caagagcta  
49 gcctgataaaa tttagaggggaa aaaaaaaaaat ctccagtccc ttcacgtcgt gacgcttgc  
51 tccgggaagc gggccggaag ccactcctcg agtctgcgtc aaacccgact tcaggggcc  
53 tcgtaaaagt gtcgtccctg tctctccgac cggccacagg tttccgccttgc cctctggcc  
55 ggggtcggca actgcaggcg tcagtttccc tcaag atg gcg gac gag gag gct  
56 Met Ala Asp Glu Glu Ala  
57 1 5  
59 gga ggt act gag agg atg gaa atc agc gcg gag tta ccc cag acc cct  
60 Gly Gly Thr Glu Arg Met Glu Ile Ser Ala Glu Leu Pro Gln Thr Pro  
61 10 15 20  
63 cag cgt ctg gca tct tgg tgg gat cag caa gtt gat ttt tat act gct  
64 Gln Arg Leu Ala Ser Trp Trp Asp Gln Gln Val Asp Phe Tyr Thr Ala  
65 25 30 35  
67 ttc ttg cat cat ttg gca caa ttg gtg cca gaa att tac ttt gct gaa  
68 Phe Leu His His Leu Ala Gln Leu Val Pro Glu Ile Tyr Phe Ala Glu  
69 40 45 50  
71 atg gac cca gac ttg gaa aag cag gag gaa agt gta caa atg tca ata  
72 Met Asp Pro Asp Leu Glu Lys Gln Glu Glu Ser Val Gln Met Ser Ile  
73 55 60 65 70  
75 ttc act cca ctg gaa tgg tac tta ttt gga gaa gat cca gat att tgc  
76 Phe Thr Pro Leu Glu Trp Tyr Leu Phe Gly Glu Asp Pro Asp Ile Cys  
77 75 80 85

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79 tta gag aaa ttg aag cac agt gga gca ttt cag ctt tgt ggg agg gtt	1001
80 Leu Glu Lys Leu Lys His Ser Gly Ala Phe Gln Leu Cys Gly Arg Val	
81 90 95 100	
83 ttc aaa agt gga gag aca acc tat tct tgc agg gat tgt gca att gat	1049
84 Phe Lys Ser Gly Glu Thr Thr Tyr Ser Cys Arg Asp Cys Ala Ile Asp	
85 105 110 115	
87 cca aca tgt gta ctc tgt atg gac tgc ttc cag gac agt gtt cat aaa	1097
88 Pro Thr Cys Val Leu Cys Met Asp Cys Phe Gln Asp Ser Val His Lys	
89 120 125 130	
91 aat cat cgt tac aag atg cat act tct act gga gga ggg ttc tgt gac	1145
92 Asn His Arg Tyr Lys Met His Thr Ser Thr Gly Gly Gly Phe Cys Asp	
93 135 140 145 150	
95 tgt gga gac aca gag gca tgg aaa act ggc cct ttt tgt gta aat cat	1193
96 Cys Gly Asp Thr Glu Ala Trp Lys Thr Gly Pro Phe Cys Val Asn His	
97 155 160 165	
99 gaa cct gga aga gca ggt act ata aaa gag aat tca cgc tgt ccg ttg	1241
100 Glu Pro Gly Arg Ala Gly Thr Ile Lys Glu Asn Ser Arg Cys Pro Leu	
101 170 175 180	
103 aat gaa gag gta att gtc caa gcc agg aaa ata ttt cct tca gtg ata	1289
104 Asn Glu Glu Val Ile Val Gln Ala Arg Lys Ile Phe Pro Ser Val Ile	
105 185 190 195	
107 aaa tat gtc gta gaa atg act ata tgg gaa gag gaa aaa gaa ctg cct	1337
108 Lys Tyr Val Val Glu Met Thr Ile Trp Glu Glu Lys Glu Leu Pro	
109 200 205 210	
111 cct gaa ctc cag ata agg gag aaa aat gaa aga tac tat tgt gtc ctt	1385
112 Pro Glu Leu Gln Ile Arg Glu Lys Asn Glu Arg Tyr Tyr Cys Val Leu	
113 215 220 225 230	
117 ttc aat gat gaa cac cat tca tat gac cac gtc ata tac agc cta caa	1433
118 Phe Asn Asp Glu His His Ser Tyr Asp His Val Ile Tyr Ser Leu Gln	
119 235 240 245	
121 aga gct ctt gac tgt gag ctc gca gag gcc cag ttg cat acc act gcc	1481
122 Arg Ala Leu Asp Cys Glu Leu Ala Glu Ala Gln Leu His Thr Thr Ala	
123 250 255 260	
126 att gac aaa gag ggt cgt cgg gct gtt aaa gcg gga gct tat gct gct	1529
127 Ile Asp Lys Glu Gly Arg Arg Ala Val Lys Ala Gly Ala Tyr Ala Ala	
128 265 270 275	
130 tgc cag gaa gca aag gaa gat ata aag agt cat tca gaa aat gtc tct	1577
131 Cys Gln Glu Ala Lys Glu Asp Ile Lys Ser His Ser Glu Asn Val Ser	
132 280 285 290	
134 caa cat cca ctt cat gta gaa gta tta cac tca gag att atg gct cat	1625
135 Gln His Pro Leu His Val Glu Val Leu His Ser Glu Ile Met Ala His	
136 295 300 305 310	
138 cag aaa ttt gct ttg cgt ctt ggt tcc tgg atg aac aaa att atg agc	1673
139 Gln Lys Phe Ala Leu Arg Leu Gly Ser Trp Met Asn Lys Ile Met Ser	
140 315 320 325	
142 tat tca agt gac ttt agg cag atc ttt tgc caa gca tgc ctt aga gaa	1721
143 Tyr Ser Ser Asp Phe Arg Gln Ile Phe Cys Gln Ala Cys Leu Arg Glu	
144 330 335 340	
146 gaa cct gac tcg gag aat ccc tgt ctc ata agc agg tta atg ctt tgg	1769

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147	Glu	Pro	Asp	Ser	Glu	Asn	Pro	Cys	Leu	Ile	Ser	Arg	Leu	Met	Leu	Trp	
148	345				350								355				
150	gat	gca	aag	ctt	tat	aaa	ggt	gcc	cgt	aag	atc	ctt	cat	gaa	ttg	atc	1817
151	Asp	Ala	Lys	Leu	Tyr	Lys	Gly	Ala	Arg	Lys	Ile	Leu	His	Glu	Leu	Ile	
152	360				365							370					
154	tcc	agc	agt	ttt	ttt	atg	gag	atg	gaa	tac	aaa	aaa	ctc	ttt	gct	atg	1865
155	Phe	Ser	Ser	Phe	Phe	Met	Glu	Met	Glu	Tyr	Lys	Lys	Leu	Phe	Ala	Met	
156	375				380						385			390			
158	gaa	ttt	gtg	aag	tat	tat	aaa	caa	ctg	cag	aaa	gaa	tat	atc	agt	gat	1913
159	Glu	Phe	Val	Lys	Tyr	Tyr	Lys	Gln	Leu	Gln	Lys	Glu	Tyr	Ile	Ser	Asp	
160	395				400							405					
162	gat	cat	gac	aga	agt	atc	tct	ata	act	gca	ctt	tca	gtt	cag	atg	ttt	1961
163	Asp	His	Asp	Arg	Ser	Ile	Ser	Ile	Thr	Ala	Leu	Ser	Val	Gln	Met	Phe	
164	410				415							420					
166	act	gtt	cct	act	ctg	gct	cga	cat	ctt	att	gaa	gag	cag	aat	gtt	atc	2009
167	Thr	Val	Pro	Thr	Leu	Ala	Arg	His	Leu	Ile	Glu	Glu	Gln	Asn	Val	Ile	
168	425				430						435						
170	tct	gtc	att	act	gaa	act	ctg	cta	gaa	gtt	tta	cct	gag	tac	ttg	gac	2057
171	Ser	Val	Ile	Thr	Glu	Thr	Leu	Leu	Glu	Val	Leu	Pro	Glu	Tyr	Leu	Asp	
172	440				445						450						
175	agg	aac	aat	aaa	ttc	aac	ttc	cag	ggt	tat	agc	cag	gac	aaa	ttg	gga	2105
176	Arg	Asn	Asn	Lys	Phe	Asn	Phe	Gln	Gly	Tyr	Ser	Gln	Asp	Lys	Leu	Gly	
177	455				460						465			470			
179	aga	gta	tat	gca	gta	ata	tgt	gac	cta	aag	tat	atc	ctg	atc	agc	aaa	2153
180	Arg	Val	Tyr	Ala	Val	Ile	Cys	Asp	Leu	Lys	Tyr	Ile	Leu	Ile	Ser	Lys	
181	475				480							485					
183	ccc	aca	ata	tgg	aca	gaa	aga	tta	aga	atg	cag	ttc	ctt	gaa	gtt	ttt	2201
184	Pro	Thr	Ile	Trp	Thr	Glu	Arg	Leu	Arg	Met	Gln	Phe	Leu	Glu	Gly	Phe	
185	490				495						500						
188	cga	tct	ttt	ttg	aag	att	ctt	acc	tgt	atg	cag	gga	atg	gaa	gaa	atc	2249
189	Arg	Ser	Phe	Leu	Lys	Ile	Leu	Thr	Cys	Met	Gln	Gly	Met	Glu	Glu	Ile	
190	505				510						515						
192	cga	aga	cag	gtt	ggg	caa	cac	att	gaa	gtg	gat	cct	gat	tgg	gag	gct	2297
193	Arg	Arg	Gln	Val	Gly	Gln	His	Ile	Glu	Val	Asp	Pro	Asp	Trp	Glu	Ala	
194	520				525						530						
196	gcc	att	gct	ata	cag	atg	caa	ttg	aag	aat	att	tta	ctc	atg	ttc	caa	2345
197	Ala	Ile	Ala	Ile	Gln	Met	Gln	Leu	Lys	Asn	Ile	Leu	Leu	Met	Phe	Gln	
198	535				540						545			550			
200	gag	tgg	tgt	tgt	gat	gaa	gaa	ctc	tta	ctt	gtg	gct	tat	aaa	gaa		2393
201	Glu	Trp	Cys	Ala	Cys	Asp	Glu	Leu	Leu	Leu	Val	Ala	Tyr	Lys	Glu		
202	555				560						565						
204	tgt	cac	aaa	gct	gtg	atg	agg	tgc	agt	acc	agt	ttc	ata	tct	agt	agc	2441
205	Cys	His	Lys	Ala	Val	Met	Arg	Cys	Ser	Thr	Ser	Phe	Ile	Ser	Ser	Ser	
206	570				575						580						
208	aag	aca	gta	gta	caa	tgc	tgt	gga	cat	agt	ttg	gaa	aca	aag	tcc	tac	2489
209	Lys	Thr	Val	Val	Gln	Ser	Cys	Gly	His	Ser	Leu	Glu	Thr	Lys	Ser	Tyr	
210	585				590						595						
212	aga	gta	tct	gag	gat	ctt	gta	agc	ata	cat	ctg	cca	ctc	tct	agg	acc	2537
213	Arg	Val	Ser	Glu	Asp	Leu	Val	Ser	Ile	His	Leu	Pro	Leu	Ser	Arg	Thr	

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214	600	605	610		
216	cct gct ggt ctt cat gta cgt tta agc agg ctg ggt gct gtt tca aga			2585	
217	Leu Ala Gly Leu His Val Arg Leu Ser Arg Leu Gly Ala Val Ser Arg				
218	615	620	625	630	
220	ctg cat gaa ttt gtg tct ttt gag gac ttt caa gta gag gta cta gtg			2633	
221	Leu His Glu Phe Val Ser Phe Glu Asp Phe Gln Val Glu Val Leu Val				
222	635	640	645		
224	gaa tat cct tta cgt tgt ctg gtg ttg gtt gcc cag gtt gtt gct gag			2681	
225	Glu Tyr Pro Leu Arg Cys Leu Val Leu Val Ala Gln Val Val Ala Glu				
226	650	655	660		
228	atg tgg cga aga aat gga ctg tct ctt att agc cag gtg ttt tat tac			2729	
229	Met Trp Arg Arg Asn Gly Leu Ser Leu Ile Ser Gln Val Phe Tyr Tyr				
230	665	670	675		
233	caa gat gtt aag tgc aga gaa gaa atg tat gat aaa gat atc atc atg			2777	
234	Gln Asp Val Lys Cys Arg Glu Glu Met Tyr Asp Lys Asp Ile Ile Met				
235	680	685	690		
237	cct cag att ggt gca tct tta atg gat ccc aat aag ttc ttg tta ctg			2825	
238	Leu Gln Ile Gly Ala Ser Leu Met Asp Pro Asn Lys Phe Leu Leu Leu				
239	695	700	705	710	
241	gta ctt cag agg tat gaa ctt gcc gag gct ttt aac aag acc ata tct			2873	
242	Val Leu Gln Arg Tyr Glu Leu Ala Glu Ala Phe Asn Lys Thr Ile Ser				
243	715	720	725		
245	aca aaa gac cag gat ttg att aaa caa tat aat aca cta ata gaa gaa			2921	
246	Thr Lys Asp Gln Asp Leu Ile Lys Gln Tyr Asn Thr Leu Ile Glu Glu				
247	730	735	740		
250	atg ctt cag gtc ctc atc tat att gtg ggt gag cgt tat gta cct gga			2969	
251	Met Leu Gln Val Leu Ile Tyr Ile Val Gly Glu Arg Tyr Val Pro Gly				
252	745	750	755		
254	gtg gga aat gtg acc aaa gaa gag gtc aca atg aga gaa atc att cac			3017	
255	Val Gly Asn Val Thr Lys Glu Glu Val Thr Met Arg Glu Ile Ile His				
256	760	765	770		
258	ttg ctt tgc att gaa ccc atg cca cac agt gcc att gcc aaa aat tta			3065	
259	Leu Leu Cys Ile Glu Pro Met Pro His Ser Ala Ile Ala Lys Asn Leu				
260	775	780	785	790	
262	cct gag aat gaa aat aat gaa act ggc tta gag aat gtc ata aac aaa			3113	
263	Pro Glu Asn Glu Asn Glu Thr Gly Leu Glu Asn Val Ile Asn Lys				
264	795	800	805		
266	gtg gcc aca ttt aag aaa cca ggt gta tca ggc cat gga gtt tat gaa			3161	
267	Val Ala Thr Phe Lys Lys Pro Gly Val Ser Gly His Gly Val Tyr Glu				
268	810	815	820		
270	cta aaa gat gaa tca ctg aaa gac ttc aat atg tac ttt tat cat tac			3209	
271	Leu Lys Asp Glu Ser Leu Lys Asp Phe Asn Met Tyr Phe Tyr His Tyr				
272	825	830	835		
274	tcc aaa acc cag cat agc aag gct gaa cat atg cag aag aaa agg aga			3257	
275	Ser Lys Thr Gln His Ser Lys Ala Glu His Met Gln Lys Lys Arg Arg				
276	840	845	850		
278	aaa caa gaa aac aaa gat gaa gca ttg ccg cca cca cca cct cct gaa			3305	
279	Lys Gln Glu Asn Lys Asp Glu Ala Leu Pro Pro Pro Pro Pro Pro Glu				
280	855	860	865	870	

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282 ttc tgc cct gct ttc agc aaa gtg att aac ctt ctc aac tgt gat atc	3353
283 Phe Cys Pro Ala Phe Ser Lys Val Ile Asn Leu Leu Asn Cys Asp Ile	
284 875 880 885	
286 atg atg tac att ctc agg acc gta ttt gag cg gca ata gac aca gat	3401
287 Met Met Tyr Ile Leu Arg Thr Val Phe Glu Arg Ala Ile Asp Thr Asp	
288 890 895 900	
291 tct aac ttg tgg acc gaa ggg atg ctc caa atg gct ttt cat att ctg	3449
292 Ser Asn Leu Trp Thr Glu Gly Met Leu Gln Met Ala Phe His Ile Leu	
293 905 910 915	
295 gca ttg ggt tta cta gaa gag aag caa cag ctt caa aaa gct cct gaa	3497
296 Ala Leu Gly Leu Leu Glu Glu Lys Gln Gln Leu Gln Lys Ala Pro Glu	
297 920 925 930	
299 gaa gaa gta aca ttt gac ttt tat cat aag gct tca aga ttg gga agt	3545
300 Glu Glu Val Thr Phe Asp Phe Tyr His Lys Ala Ser Arg Leu Gly Ser	
301 935 940 945 950	
303 tca gcc atg aat ata caa atg ctt ttg gaa aaa ctc aaa gga att ccc	3593
304 Ser Ala Met Asn Ile Gln Met Leu Leu Glu Lys Leu Lys Gly Ile Pro	
305 955 960 965	
307 cag tta gaa ggc cag aag gac atg ata acg tgg ata ctt cag atg ttt	3641
308 Gln Leu Glu Gly Gln Lys Asp Met Ile Thr Trp Ile Leu Gln Met Phe	
309 970 975 980	
312 gac aca gtg aag cga tta aga gaa aaa tct tgt tta att gta gca acc	3689
313 Asp Thr Val Lys Arg Leu Arg Glu Lys Ser Cys Leu Ile Val Ala Thr	
314 985 990 995	
316 aca tca gga tcg gaa tct att aag aat gat gag att act cat gat	3734
317 Thr Ser Gly Ser Glu Ser Ile Lys Asn Asp Glu Ile Thr His Asp	
318 1000 1005 1010	
320 aaa gaa aaa gca gaa cga aaa aga aaa gct gaa gct gct agg cta	3779
321 Lys Glu Lys Ala Glu Arg Lys Arg Lys Ala Glu Ala Ala Arg Leu	
322 1015 1020 1025	
324 cat cgc cag aag atc atg gct cag atg tct gcc tta cag aaa aac	3824
325 His Arg Gln Lys Ile Met Ala Gln Met Ser Ala Leu Gln Lys Asn	
326 1030 1035 1040	
328 ttc att gaa act cat aaa ctc atg tat gac aat aca tca gaa atg	3869
329 Phe Ile Glu Thr His Lys Leu Met Tyr Asp Asn Thr Ser Glu Met	
330 1045 1050 1055	
332 cct ggg aaa gaa gat tcc att atg gag gaa gag agc acc cca gca	3914
333 Pro Gly Lys Glu Asp Ser Ile Met Glu Glu Ser Thr Pro Ala	
334 1060 1065 1070	
336 gtc agt gac tac tct aga att gct ttg ggt cct aaa cgg ggt cca	3959
337 Val Ser Asp Tyr Ser Arg Ile Ala Leu Gly Pro Lys Arg Gly Pro	
338 1075 1080 1085	
340 tct gtt act gaa aag gag gtg ctg acg tgc atc ctt tgc caa gaa	4004
341 Ser Val Thr Glu Lys Glu Val Leu Thr Cys Ile Leu Cys Gln Glu	
342 1090 1095 1100	
344 gaa cag gag gtg aaa ata gaa aat aat gcc atg gta tta tcg gcc	4049
345 Glu Gln Glu Val Lys Ile Glu Asn Asn Ala Met Val Leu Ser Ala	
346 1105 1110 1115	
349 tgt gtc cag aaa tct act gcc tta acc cag cac agg gga aaa ccc	4094

→ Use of n and/or Xaa has been detected in the Sequence Listing.  
 Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

**VERIFICATION SUMMARY**

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L:2834 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18